

Reference and troubleshooting guide



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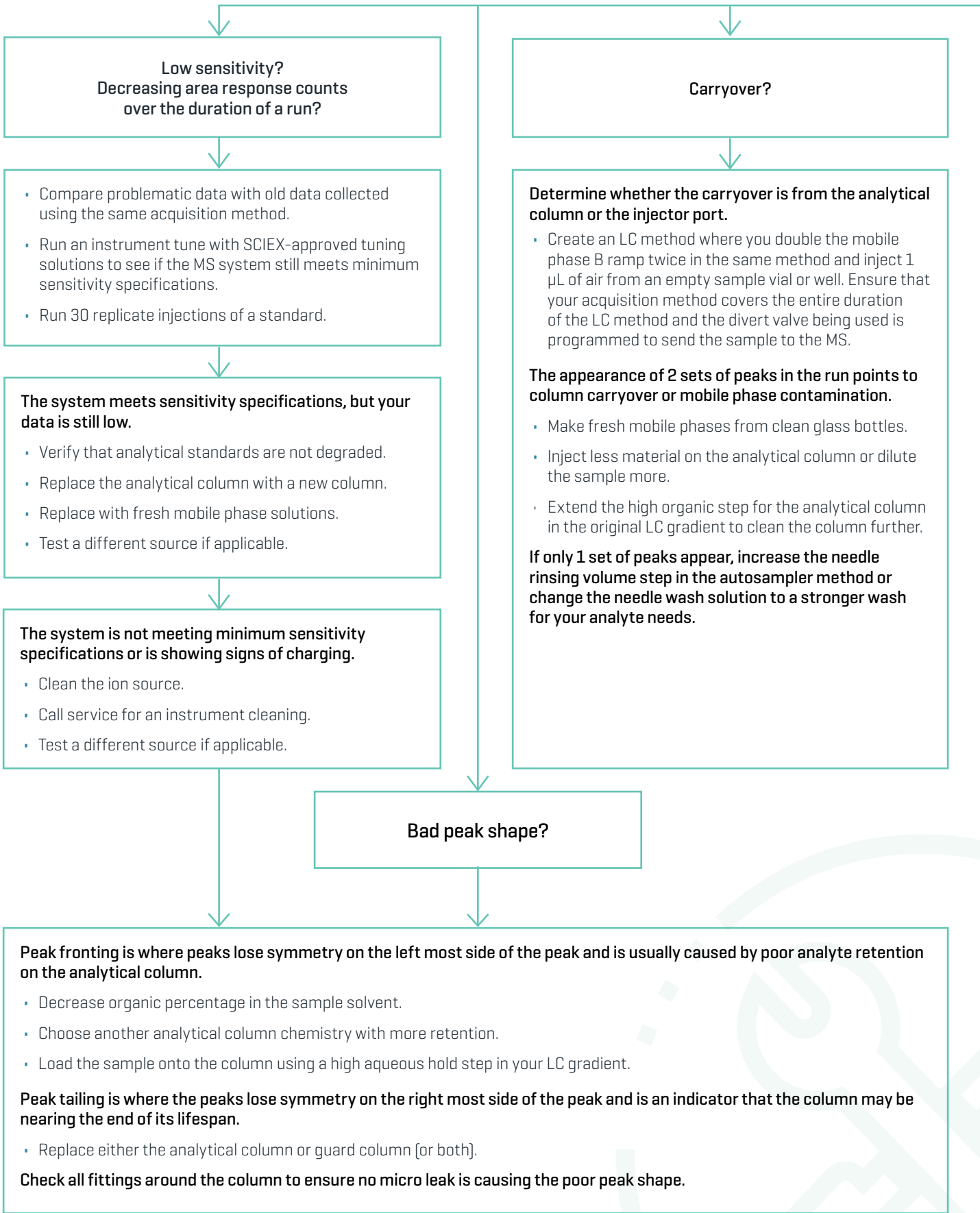
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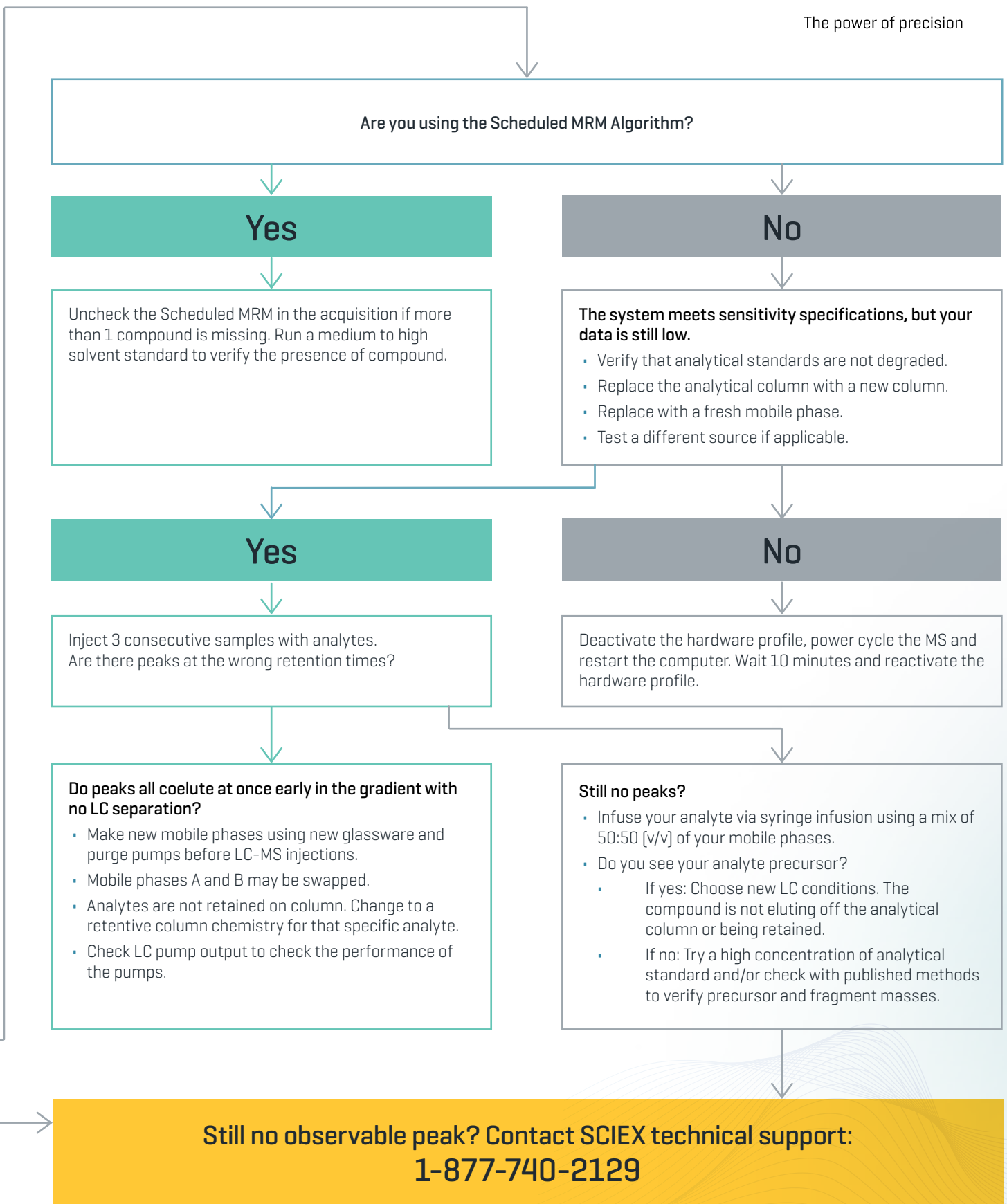
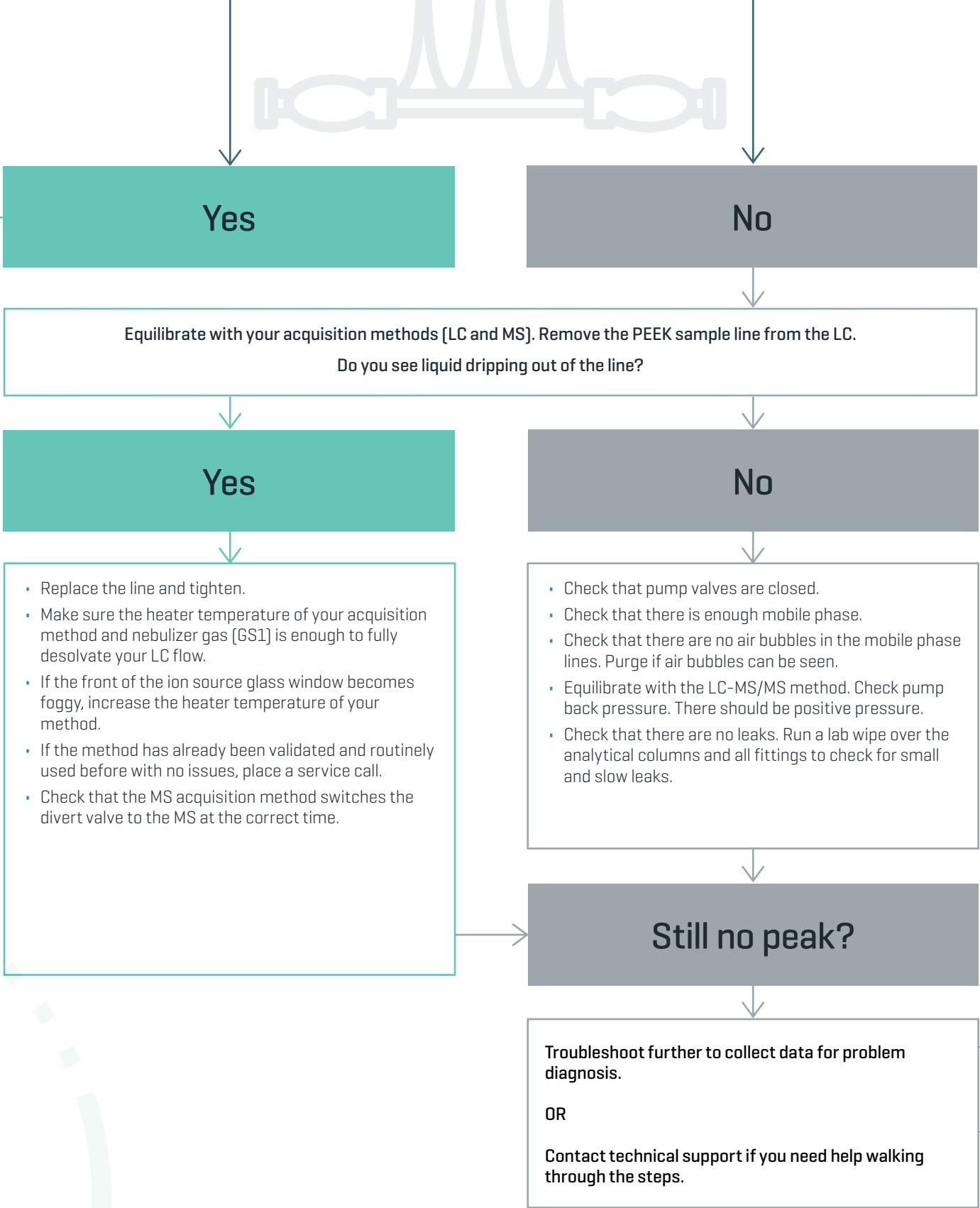
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Troubleshooting

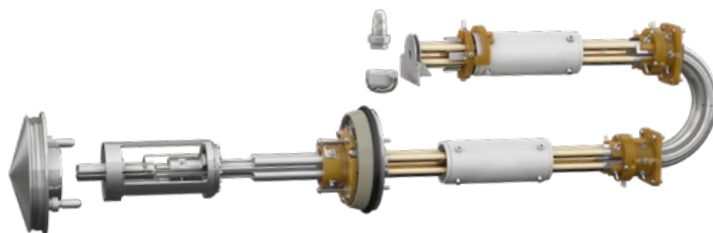


Do you see a peak?



Triple quadrupole technology

Triple quadrupole mass spectrometers have long been the benchmark for quantitation due to their sensitivity and specificity. Combined with SCIEX QTRAP technology, a triple quadrupole mass spectrometer can also be used as a linear ion trap [LIT] for even more sensitivity and selectivity.



Triple quadrupole scans

Multiple reaction monitoring [MRM]:

- MRM scans select specific precursor ions and fragment them to monitor specific productions.
- These scans are generally used for quantitation of a targeted list of compounds.

Precursor ion:

- With this scan, the third quadrupole [Q3] is set to a fixed mass and the first quadrupole [Q1] sweeps a mass range. It scans for the ion of a specific mass-to-charge ratio that is generating specific product ions.

Product ion:

- A product ion experiment searches for all of the products of a particular precursor fragmenting in the second quadrupole [Q2].
- It is generally used for compound optimization to determine product ions.

Neutral loss:

- This is a survey scan to monitor precursor ions that have a specific neutral loss.

Q1/Q3 full scan:

- This type of scan utilizes Q1 or Q3 as a mass filter to scan across a mass range or focus on certain ions with a specific mass window width.
- It is generally used to determine precursor masses for compound optimization.

QTRAP system scans

Enhanced MS [EMS]:

- With an EMS scan, a specified precursor ion mass is trapped in the LIT before being released to the detector.

Enhanced resolution [ER]:

- With an ER scan, ions within a 20 Da region are collected in the LIT for a specified fill time and scanned out slowly for enhanced resolution.

Enhanced product ion [EPI]:

- An EPI scan is a triple quadrupole MS/MS scan where product ions are trapped in the LIT before hitting the detector.

Enhanced multiply charged [EMC]:

- This is an MS scan in which multiply charged ions are detected within the specified range.

MS/MS/MS [MS³]

- With MS³ scans, product ions of a specified m/z are isolated in the LIT and further fragmented. The resulting fragment ions are trapped into the LIT prior to being scanned out and detected.

Information dependent acquisition [IDA]:

- An IDA experiment analyzes data as it is being acquired and changes experiment conditions according to the results of the analysis. It determines the masses on which to perform dependent scans.

Accurate mass technology

QTOF mass spectrometers combine quadrupole with time-of-flight technology, where ions travel through a flight tube to determine ion mass at high resolution, along with mass accuracy below 5 ppm. Fast scan speeds are necessary to maintain product ion resolution for enhanced spectral library matching.

QTOF scans

Information dependent acquisition (IDA):

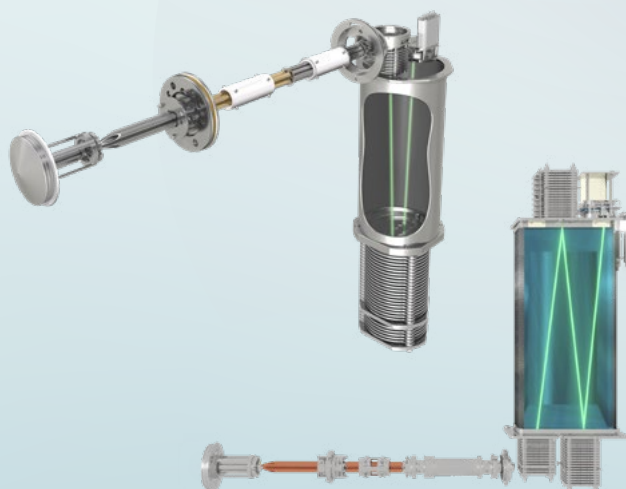
- An IDA experiment analyzes data as it is being acquired and changes experimental conditions according to the results of the analysis. Analysis of the results determines the masses on which to perform dependent scans. The user has total control over the criteria that activates an IDA experiment and the parameters of the IDA experiment that are activated.

SWATH Acquisition:

- With this type of scan, the MS uses a specified Q1 isolation window and steps it across the entire m/z mass detection range, collecting full MS/MS spectra on every detectable analyte that passes through each Q1 window.
- With SWATH Acquisition, MS/MS data is never missed even if the peak signal intensity is low within a given mass window.

MRM^{HR}:

- With MRM^{HR} scans, MS/MS data is acquired from compounds with known masses and retention times with maximum selectivity. This acquisition can also be used to extract fragment masses with narrow widths [0.02 Da] from TOF MS/MS spectra.



Screening workflows

Targeted screening

- Compounds verified with analytical standards
- Highest confidence in compound ID

Suspect screening

- No analytical standards
- Spectral library matching with mass accuracy
- Analyte peak chosen based on molecular formula or target mass

Nontargeted screening

- No analytical standards
- Spectral library matching with mass accuracy
- Analyte peaks are all evaluated if minimum peak integration criteria is met

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